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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: 

Title: Perfect score: US-09-331-631A-3\_COPY\_117\_185 384 .

Sequence: 1 NRQRDPQQQYEQCQERCQRH.....EEQQREDEEKYEERMKEEDN 69

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 88757 segs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Ĺ	J W	, ω , μ	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	1.4	13	12	11	10	9	œ	7	6	. 5	4	w	2	1	NO.	Result
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	P13050 streptococc					plasmodiu	pisum sat	dictyo	rattu	homo sapi	=	homo	sacch			drosc		ω	œ	7 drosophíl	N	מ	_	2 glycine	1 macac	93074 homo	34099 dicty	15696 homo	709 oryctola	283 homo sapie	799 dossypium	01 qos	Description	

Dр Qy Db QΥ

1 NRORDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEBQQ------- 53
:| |||::||:||: || || ||||| ||:|::|| |
78 HRPEDPQRRYEECQQECR--QQEERQRPQCQQRCLKRPEQEQQQSQRQFQEQEQQHCHQQE 135

45	44	43	42	41	40	39 .	38	37	36	35	34
83	83.5	83.5	83.5	84	84.5	85	85	85	85	85.5	85.5
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P16947 streptococc	٠,	-	φ.	Ψ.	۷.		٠,	-	P18174 canis famil	·	٠,

## ALIGNMENTS

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RESULT 2
VCLA_GOSHI
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Best Local
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Q07283;
Q1-OCT-1994
Q1-OCT-1994
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                            HUMAN
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P09799;
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Sequences and genomic organization of the colonilin fulfilm account for the colonilin fulfilm account for the colonilin fulfilm account for the coloniling fulfilm account fulfilm account for the coloniling fulfilm account fulfilm account for the coloniling fulfilm account 
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Gossypium hirsutum (Upland cotton).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                    THH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   globulin (vicilin) genes of cottonseed.";
Plant Mol. Biol. 9:533-546(1987).
-i- FUNCTION: SEED STORAGE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
MEDLINE=93280194;
                                                                                                 Eukaryota;
                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                        TRICHOHYALIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                              OR TRHY OR THL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  storage protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00546; Seedstore_7s;
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25; Conser
                      FROM
                                                                       Eutheria;
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  PubMed=7685034
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                                                                       Chordata;
Primates;
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Last annotation updat
                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 133; DB 1; I
Pred. No. 0.00028;
8; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VICILIN
                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             197
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C9DB9371C976953B CRC64;
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Lee S.-C., Kim I.-G., Marekov L.N., O'Keefe E.J., Parry D.A.D., Steinert P.M.;
"The structure of human trichohyalin. Potential multiple roles as a functional EF-hand-like calcium-binding protein, a cornified cell envelope precursor, and an intermediate filament-associated (cross-linking) protein.";
J. Biol. Chem. 268:12164-12176(1993).
                REPEAT
REPEAT
                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                           PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIFFERENTIATION.
-!- SUBUNIT: MONOMER (PROBABLE).
-!- TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES S
-!- THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AN
THE FILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE)
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermis."
J. Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Keefe E.J., Hamilton E.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1731-1898
MEDLINE=93315897; Pub
                                                                                                          DOMAIN
                                                                                                                                            CA_BIND
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                  Repeat;
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PROSITE; PS00303; S100_CABP;
                                                                                                                                                                                                                                        PFAM;
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                                                                                                                                                                                                                                                                                                               MIM; 190370;
                                                                                                                                                                                                                                                                                                                                               EMBL; L09190; AAA65582.1; PIR; A45973; A45973.
                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                              HSSP; P02633; 1BOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINCLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAIN 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN DIFFERENT SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIFEDTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED. IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARI PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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RPRO; IPRO02048; -.
I; PF01023; S_100; 1.
I; PF00036; efhand; 1.
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                                                                                                                                                                              Calcium-binding.
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314
327
340
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365
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PubMed=7686953;
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                                                  SITE I (LOW AFFINITY) (POTENTIAL).
SITE II (HIGH AFFINITY) (POTENTIAL).
SITE II (HIGH AFFINITY) (POTENTIAL)
6 X 13 AA TANDEM REPEATS OF
R-R-E-Q-E-E-R-R-B-Q-Q-L.
1-1 (APPROXIMATE).
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1-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND CHARACTERIZATION
                                   (APPROXIMATE)
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OF PEPTIDE REPEATS
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Best Local
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                                                                                                            Fietz M.J., Rogers G.E.;

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERNIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPETPIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK.
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Eukaryota; Metazoa; Chordata; (
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01-OCT-1994
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                                 SUBUNIT: HOMODIMER (PROBABLE).
TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES S
THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AN
THE FILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE)
              DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION
                                                                                                         DIFFERENTIATION.
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OERDROYR -> RSETGSTG (IN REF. 2).

Q -> K (IN REF. 2).

V -> G (IN REF. 2).

WW; A74B5947FB62E31D CRC64;
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Pred.
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ID U2R2_HUMAN
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR
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CA_BIND
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SEQUENCE
                                                        MEDLINE=96163878; PubMed=8586425;
Kitagawa K., Wang X., Hatada I.,
Inazawa J., Abe T., Mitsuya K., O
                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR001751; -. INTERPRO; IPR002048; -. PFAM; PF01023; S_100; 1.
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                             Mukai T
                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         U2AF1-RS2 OR U2AF1RS2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
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27; Conserv
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SITE I (LOW AFFINITY) (POTENTIAL).
SITE II (HIGH AFFINITY) (POTENTIAL).
MW; AE17D2A159F12B7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110; DB:
Pred. No. 0.04;
9; Mismatches
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                                                                   Oshimura
                                                                                                        Yamaoka
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                                                               Nojima
Murata
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P34099;
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Genomics 30:257-263(1995).
-i- SUBCELULAR LOCATION: NUCLEAR (POTENTIAL).
-i- SUBCELULAR LOCATION: NUCLEAR (POTENTIAL).
-i- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
MEDLINE=93066311; PubMed=1332055; Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.; Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.; PDdPK3, which plays essential roles during Dictyostelium development, encodes the catalytic subunit of cAMF-dependent protein kinase."; Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buerki E., Anjard C., Scholder J.-C., Reymond C.D.; "Isolation of two genes encoding putative protein kinases during Dictyostelium discoideum development.";
                                                                                                                                                                                       STRAIN-AX3
                                                                                                                                                                                                                        CHARACTERIZATION
                                                                                                                                                                                                                                                                                        Biochemistry
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                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93385090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91323730;
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Dictyostelium discoideum
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Nuclear protein; Ribonucleoprotein
DOMAIN 46 49 POLY-
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PFAM; PF00642; zf-CCCH; 1.
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                                                                                                                                                                                                                                                                                                                  jard C., Etchebehere L., Pinaud n unusual catalytic subunit for Dictyostelium discoideum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300028;
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482 AA;
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39,
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58044 MW; IDACC8A6CA4727A6 CRC64;
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Q1-NOV-1997 (Rel. 3
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DOMAIN 58
DOMAIN 136
DOMAIN 233
DOMAIN 336
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BINDING 365
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MOD_RES
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            TISSUE=BONE MARROW,
                       SEQUENCE FROM N.A
                                                 Mammalla;
                                                              Eukaryota; Metazoa;
                                                                          HOMO
                                                                                       KIAA0192
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00107
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HSSP; P05132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
MEDLINE=96281124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A MAXIMUM AT CULMINATION. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAMP SUBFAMILY.
                                                                        sapiens
                                                                                                                                                                                                                                                  DEEKYEERMKEE
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17; Conserv
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                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                           648
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                              (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
PROTEIN KIAAO192 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein kinase; ATP-binding; cAMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JQ1150.
                                                                          (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pkinase_C; 1.
07; PROTEIN_KINASE_ATP;
                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                          215
PubMed=8724849;
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PROTEIN_KINASE_DOM;
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223
250
590
350
365
459
                                                 Primates;
                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
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ATP (BY SIMILARITY).
BY SIMILARITY.
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9; Mismatches
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THR-RICH.
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Pred. No. 0.19;
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                                                 Catarrhini;
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                    APA4_MACFA P33621;
                                                                                                                                  "Nucleotide sequences of the Macaca fascic and A-IV genes.";
Biochim. Blophys. Acta 1172:335-339(1993).
                                                                                                                                                                                                                                                                    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                   APOA4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; "Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0161-KIAA0200) of analysis of cDNA clones from human cell Line KG-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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           TISSUE SPECIFICITY: SECRETED IN PLASMA.

DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
                                                                            FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJ COMPONENT OF HDL AND CHYLOMICRONS.
SUBCELLULAR LOCATION: EXTRACELLULAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 21.4
15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires a license agreement (See http://www.isb-sib.ch/announce/
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LIPID-BINDING DOMAINS
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                                                                                                                                                                       Schaefer E.J., Ordovas J.M.; fascicularis apolipoprotein C-III
                                                                                                                                                                                                                                                                                                                                                                                                 429
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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REPEAT
REPEAT
           -!- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
-!- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE
SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDI
                                                                                                   Grimes H.D., Overvoorde P.J., Ripp K., Franceschi "A 63-kD sucrose binding protein is expressed and tissues actively engaged in sucrose transport."; Plant Cell 4:1561-1574(1992).
                                                                                                                                                                                                                                                                        Magnoliophyta; eudicotyledons; core eudicots; Fabales; Fabaceae; Papilionoideae; Glycine.
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01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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nes 19; Conserv
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SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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29, Last sequence of the contract of the contract
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
CASEIN KINASE I HOMOLOG 1 (EC 2.7.1.-).
YCK1 OR CKI2 OR YHR135C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Robinson L.C., Hubbard E.J.A., Graves P.R., de Paoli-Roach A Roach P.J., Kung C., Haas D.W., Hagedorn C.H., Goebl M., Culbertson M.R., Carlson M.; Tarlson M.; "Yeast casein kinase I homologues: an essential gene pair."; Proc. Natl. Acad. Sci. U.S.A. 89:28-32(1992).
                                         STRAIN-S288C / AB972;
MEDLINE-94378003; Pub
                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                                                                                                  MEDLINE=92329995;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92108037; PubMed=1729698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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       Johnston
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                                                                                                                                                                                  casein kinase-1.";
1. Biol. Cell 3:275-286(1992)
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DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECT
UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER
FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30
DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European
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                                                                                                                                                                                                                                                      P.-C., Vancura A., Mitc
genes in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEQD 106
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                                         PubMed=8091229;
                                                                                                                                                                                                                                                                                                                              PubMed=1627830;
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       s.
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           Brinkman
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J.,
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membrane-bound
   Ding
   Η.,
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Best Local Similarity
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PIR; S29521;
PIR; S48979;
                                                                                                                                                                                                                                                                                                         CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Iraqui I., Vissers S., Cartiaux M., Urrestarazu A.;
"Characterisation of Saccharomyces cerevisiae AROB and ARO9 genes encoding aromatic aminotransferases I and II reveals a new aminotransferase subfamily.";
MO1. Gen. Genet. 257:228-248(1998).
MO1. Gen. Genet. 257:228-248(1998).
PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
PIR; I
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SGD; S0001177; YCK1.
INTERPRO; IPR000719; -.
INTERPRO; IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M74552; AAA35229.1; -. EMBL; X6327; CAA42897.1; -. EMBL; X13625; CAA73948.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
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PROSITE; PS00107; PROTEIN_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
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AS SUBSTRATES.
SUBCELLULAR LOCATION: PLASMA-MEMBRANE BOUND.
SUBCELLULAR LOCATION: PLASMA-MEMBRANE BOUND.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
CASEIN KINASE I SUBFAMILY.
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                                                                                               QQQQQQQYAQKTEADMRNSQYKPKLDPTSYEAYQHQTQQKYLQEQQKRQQQQKLQEQQL 462
                                                                                                                                                                                                                                                                                                                                                             TE; PSO0107; PROTEIN_KINASE_ATP; 1.
TE; PSO0108; PROTEIN_KINASE_DOM; 1.
TE; PSO0108; PROTEIN_KINASE_DOM; 1.
TE; PSO011; PROTEIN_KINASE_DOM; 1.
TE; PSO0101; PROTEIN_KINASE_DOM; 1.
Extraction_treening; prenylation; Lipoprotein.
Jene family; Membrane; Lipoprotein.
Jene family; Mem
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538 AA;
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S48979.
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                                                67
                                                                                                                                                                                                             24.9%;
                                                                                                                                                                                                                                                                                                            MW.
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Pred. No. 0.
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K -> E (IN REF. 2).
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J. 26;
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Best Local S
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01-JAN-1990
15-JUL-1999
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01-OCT-1996 (Rel.
30-MAY-2000 (Rel.
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DOMAIN
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         SEQUENCE FROM N.A.
MEDLINE=94012983; PubMed=8408220;
MACKAY A.M., Eckley D.M., Chue C.,
MACKAY A.M., Eckley D.M., INCENPS
                                                                                     Gallus gallus (Chicken)
Eukaryota; Metazoa: Cho
                                                                                                                                                        INCE_CHICK P53352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol.
                                                                             Archosauria;
                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
310-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J03998; AAA29605.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid-rich protein (GARP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of a Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kemp D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89040048; PubMed=2903445; Triglia T., Stahl H.-D., Crewther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium
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                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
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(Rel. 13, Last sequence up
(Rel. 38, Last annotation
ID-RICH PROTEIN PRECURSOR.
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                                                                                                                                                                   STANDARD;
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          D.M., Chue C., of the INCENPS
                                                                            Neognathae;
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required
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7 X APPROXIMATE
for
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; Galliformes;
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association with microtubules
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                     Earnshaw W.C.;
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emosporida; Plasmodium.
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          centromere proteins):
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RESULT 13
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Best Local :
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15-DEC-1998
01-OCT-2000
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VARIANT
VARIANT
                                                  SEQUENCE rkow w.a.

MEDLINE-9626941; PubMed-8682312;

Nambu J.R., Chen W., Hu S., Crews S.T.;

"The Drosophila melanogaster similar bHLH-PAS gene encodes

"The Drosophila melanogaster similar bHLH-PAS gene encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
or send a
                           single-minded.";
Gene 172:249-254(1996)
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Cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                during interphase and with the central spindle during anaphase."; J. Cell Biol. 123:373-385(1993).
-i- FUNCTION: MAY ACT AS CYTOSKELETAL PROTEINS THAT ARE POTENTIAL
                                                                                                                                                            Eukaryota;
Pterygota;
                                                                                                                                                                                                         SIMA.
                                                                                                                                                                                                                       SIMILAR PROTEIN.
                                                                                                                                                                                                                                                                                           SIMA_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell cycle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NETWORK DURING INTERPHASE.
SUBUNIT: HOMODIMER OR HETERODIMER
SUBCELLULAR LOCATION: NUCLEAR. IS
               FUNCTION:
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Z25420; CAA80907.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                          melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
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40, Last annotation
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Pred. No. 0.47
18; Mismatches
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DIMERIZATION WITH ANOTHER
                                                                                                                                                            Brachycera; Muscomorpha;
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RESULT 14
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Best Local
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GLT_DROME STAN
p33438;
01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
30-MAY-2000 (Rel. 3
GLUTACTIN PRECURSOR
GLT.
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SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN THE EMBRYO.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
TRANSCRIPTION FACTORS. HIGHEST TO HIF-1 ALPHA.
TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outs' European Bioinformatics Institute. There are no restrictions by non-prefit institutions as long as its content is in
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SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN
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           PRECURSOR
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Schizosaccharomyces
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INTERPRO; IPRO02018; -.
PFAM; PF00135; COGSterase; 2.
PFAM; PS00941; CARBOXYLESTERASE_B_2; 1.
CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X53286; CAA37380.1;
HSSP; P21836; IMAH.
FLYBASE; FBgn0001114; Glt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Glutactin, a novel Drosophila basement membrane-related glycoprotein with sequence similarity to serine esterases."; EMBO J. 9:1219-1227(1990).
-i- FUNCTION: NOT KNOWN. BINDS CALCIUM IONS.
-i- SUBCELLULAR LOCATION: BASEMENT MEMBRANES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
[1]
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olson P.F., Fessler L.I., Nelson R.E., Sterne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN=OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: EXTENSIVELY O-GLYCOSYLATED AND ALSO N-GLYCOSYLATED -!- PTM: FOUR TYROSINES ARE SULFATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90214632; PubMed=2108864;
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33, Last sequence update)
34, Last annotation update)
9 KDA PROTEIN C29E6.10C IN C
Ascomycota; Schizosaccharomycetales;
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BY SIMILARITY.
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6; Mismatches
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WITH TYPE-B CARBOXYLESTERASE/LIPASES
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                                     CHROMOSOME
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DOMAIN 33 46
DOMAIN 184 194
DOMAIN 695 698
DOMAIN 714 717
DOMAIN 718 721
DOMAIN 938 941
SEQUENCE 1085 AA; 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones L., Murphy L., McNeil A., Simpson I., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                        EMBL; 266525; CAA91432.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972
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                                                                                                                                                     2 RQRDPQQQYEQC-QERCQRHETE-------PRHMQTCQQCCERRYEKEKRKQQK 47 ::|| ::| ::| ::|: |:|:
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